



(Seq. ID No. 1) Ssp I
GGGAAATTGTAAGCGTTAATATTTGTTAAAATTGCCTTAAATTTTGTTAAATCAGC 59

PsI
TCATTTTAACCAATAGGCCGAAATCGGCAAATCCCTTATAAATCAAAGAACGAC 118

CGAGATAGGGTTGAGTGTTCCAGTTGGAACAGAGTCCACTATTAAAGAACGTGG 177

Drd I Ade I
ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTAGTGAACCA 236

TCACCCCTAATCAAGTTTGGGTGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAA 295

NgoM IV Nae I
AGGGAGCCCCGATTAGAGCTTGACGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAG 354

BsrB I Mbi I
GGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGC 413

Fig. 4A

GTAACCACCAACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTT 472

TCGGGGAAATGTGCGCGGAACCCCTATTGTTATTTCTAAATACATTCAAATATGT 531

BsrB I
Mbi I
BspH I
Bci VI
ATCCGCTCATGAGACAATAACCCCTGATAAATGCTTCATAATATTGAAAAAGGAAGAGT 590

Ssp I Ear I

ATGAGTATTCAACATTCGCGCCCTTATTCCCTTTTGCGGCATTTCGCTTCC 649

Amp frag

Alw44 I
ApaL I
TGTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGTG 708

Amp frag

BssS I
Eco57 I
CACGAGTGGGTTACATCGAACTGGATCTAACAGCGGTAAGATCCTTGAGAGTTTCGC 767

Amp frag

Fig. 4B

Aci II
 Xmn I

CCCGAAGAACGTTTCCAATGATGAGCACTTCGACCGAATAAAACCTGTGACGGAA 826

Amp frag

GATCACTTCGCAGAATAAAATCCTGGTGCCCTGTTGATACCGGGAGGCCCTGGGC 885

BsmB I
 Van91 I Esp3 I

CAACTTTGGCGAAAATGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTACCATA 944

Bpu10 I

ATGAAATAAGATCACTACCGGGCGTATTTTGAGTTGTCGAGATTTCAGGAGCTAAG 1003

GAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCAATGGCA 1062

Chloramphenicol transferase

TCGTAAAGAACATTGAGGCATTCAGTCAGTTGCTCAATGTACCTATAACCAGACCG 1121

Chloramphenicol transferase

Fig. 4C

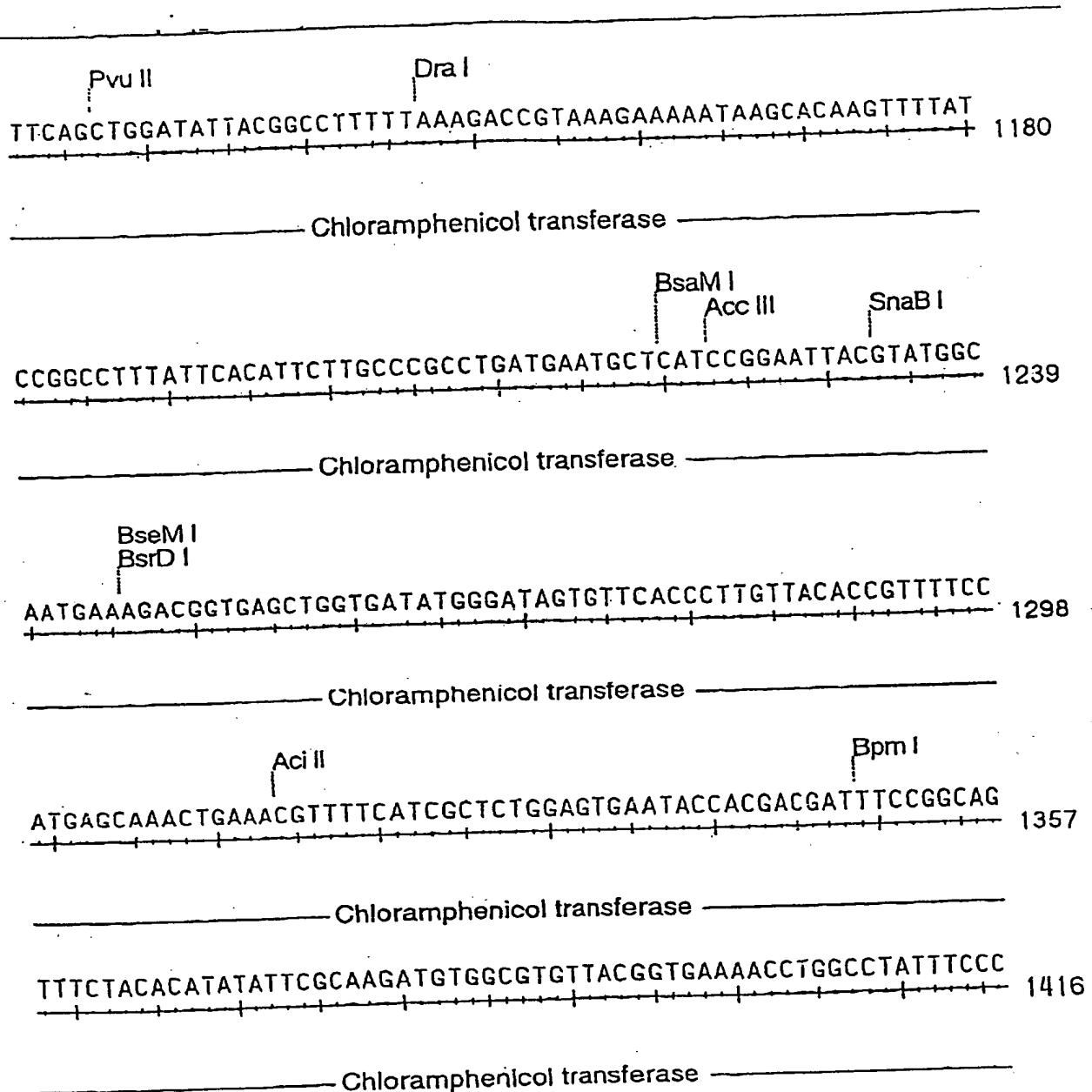


Fig. 4D

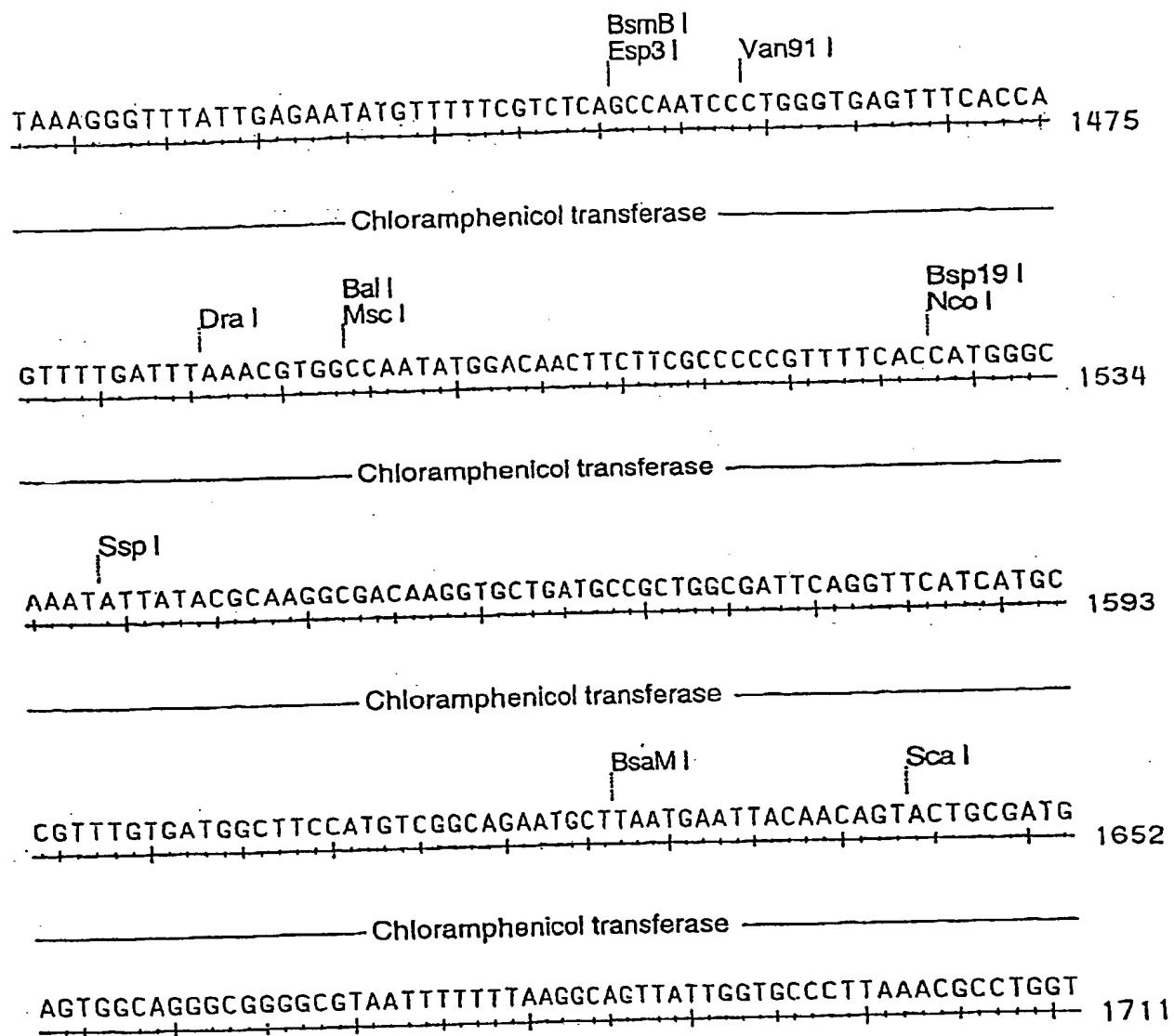


Fig. 4E

BstB1
 Csp45 I

TGCTACGCCCTGAATAAGTGATAATAAGCGGATGAATGGCAGAAATTGAAAGCAAATTC 1770

Tth111 I
 Drd I

GACCCGGTCGTCGGTTCAAGGGCAGGGTCGTTAAATAGCCGCTTATGTCTATTGCTGGTT 1829

AgeI
 PinA I

TACCGGTTTATTGACTACCGGAAGCAGTGTGACCGTGTGCTTCTCAAATGCCTGAGGCC 1888

Bpu10 I

AGTTTGCTCAGGCTCTCCCCGTGGAGGTAATAATTGACGATATGATCCTTTTTCTGA 1947

BspH I

TCAAAAAGGATCTAGGTGAAGATCCTTTGATAATCTCATGACCAAAATCCCTTAACG 2006

TGAGTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAG 2065

Bcl I

ATCCTTTTTCTGCGCGTAATCTGCTGCTTGCACAAACAAAAAAACCACCGCTACCGCG 2124

ori

Fig. 4F

Eco57 I

GTGGTTTGTGCGGATCAAGAGCTACCAACTCTTTCCGAAGGTAACGGCTTCAG 2183
ori

CAGAGCGCAGATAACAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTCA 2242
ori

AlwN I

AGAACTCTGTAGCACCGCCTACATACCTCGCTTGCTAATCCTGTTACCGAGTGGCTGCT 2301
ori

GCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAA 2360
ori

Alw44 I
ApaL I

GGCCAGCGGTGGGCTGAACGGGGGTTCGTGCACACAGCCCAGCTGGAGCGAACGA 2419
ori

CCTACACCGAACTGAGATAACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCGAA 2478
ori

Fig. 4G

The diagram illustrates a DNA sequence with various restriction enzyme recognition sites and origin of replication (ori) regions. The sequence is represented by horizontal lines with vertical tick marks indicating cleavage sites.

- Bcl VI**: Indicated above the first sequence at position 2537. The sequence is: GGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGEGCACGAG.
- BssSI**: Indicated above the second sequence at position 2596. The sequence is: GGAGCTTCCAGGGGAAACGCCCTGGTATCTTATAGTCCTGTCGGGTTTCGCCACCTCT.
- ori**: Indicated below the first and second sequences.
- DrdI**: Indicated above the third sequence at position 2655. The sequence is: GACTTGAGCGTCGATTTTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCC.
- ori**: Indicated below the third sequence.
- BspLU11I**: Indicated above the fourth sequence at position 2714. The sequence is: AGCAACGCGGCCTTTACGGTTCTGGCCTTTGCTGGCCTTTGCTCACATGTTCTT.
- ori**: Indicated below the fourth sequence.
- Tc**: Indicated above the fifth sequence at position 2773. The sequence is: TCCTGCCTTATCCCCTGATTCTGGATAACCGTATTACCGCCTTGAGTGAGCTGATA.
- BsrB I**
Mbi I: Indicated below the fifth sequence.
- Ear I**
Sap I: Indicated below the fifth sequence.
- CCGCTGCCCGAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAG**: The sequence at position 2832.

Fig. 4H

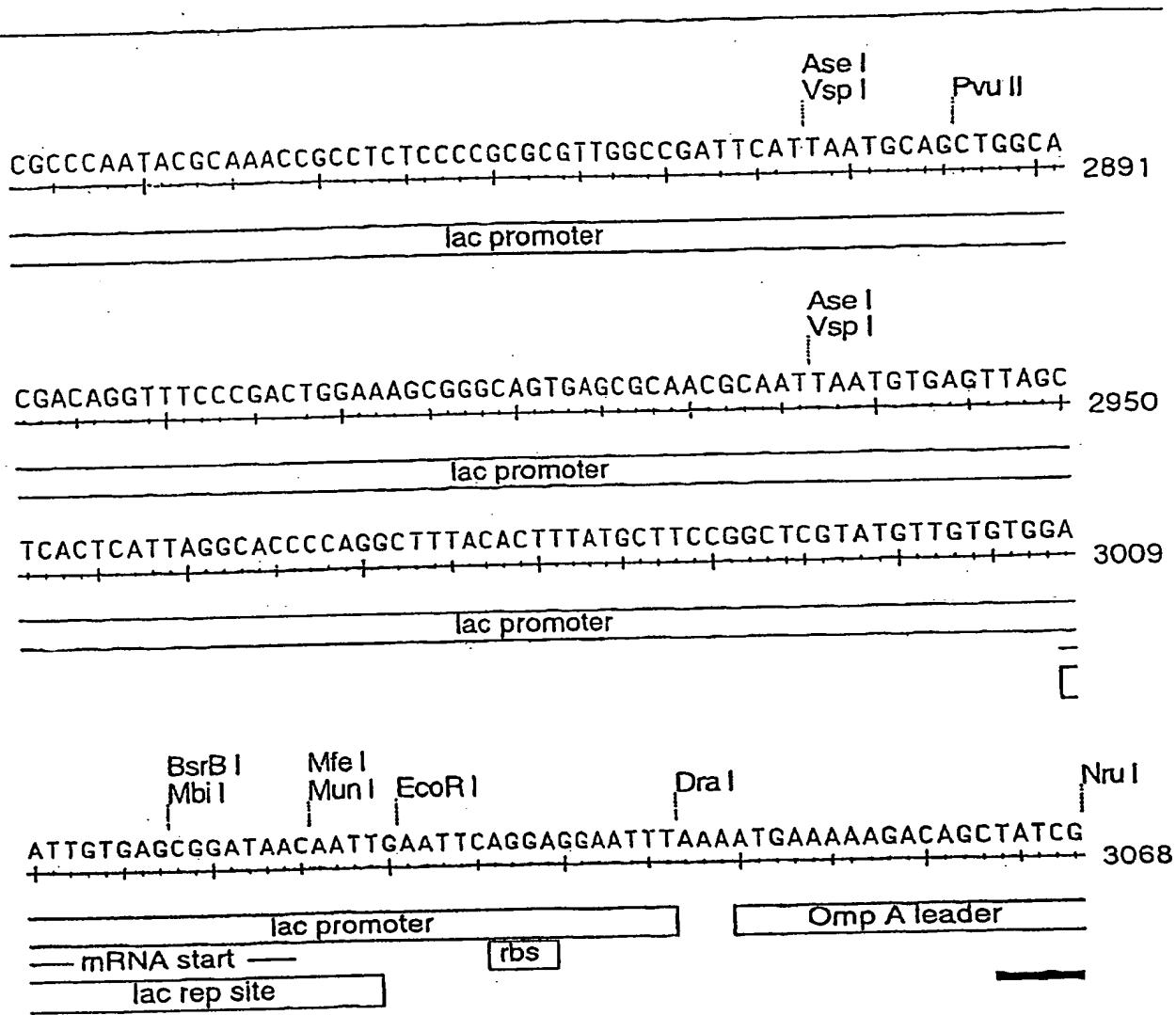


Fig. 41

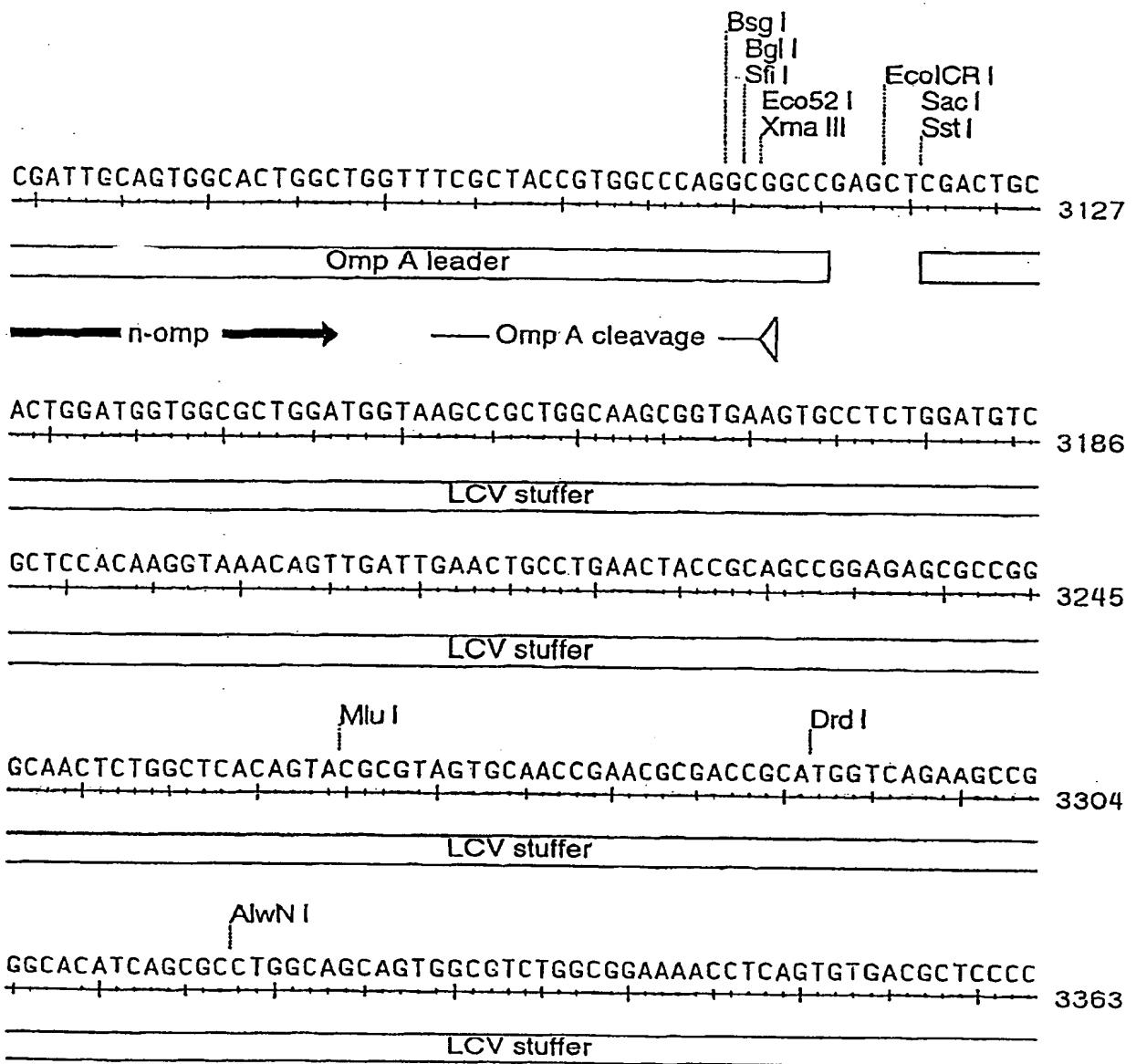


Fig. 4J

Xcm I
 BstX I

GCCGCGTCCCACGCCATCCGCATCTGACCACCAAGCGAAATGGATTTCGATCGAGCT

3422

LCV stuffer

Bgl I

GGGTAATAAGCGTTGGCAATTAAACCGCCAGTCAGGCTTCTTCACAGATGTGGATTG

3481

LCV stuffer

Alw44 I
 ApaL I

GCGATAAAAAACAAC TGCTGACGCCGCTGCGCGATCAGTTCACCCGTGCACCGCTGGAT

3540

LCV stuffer

AACGACATTGGCGTAAGTGAAGCGACCCGCATTGACCTAACGCCCTGGGTGAAACGCTG

3599

LCV stuffer

Alw44 I
 ApaL I

GAAGGCGGCGGGCCATTACCAAGGCCGAAGCAGCGTTGTCAGTGCACGGCAGATAACAC

3658

LCV stuffer

Fig. 4K

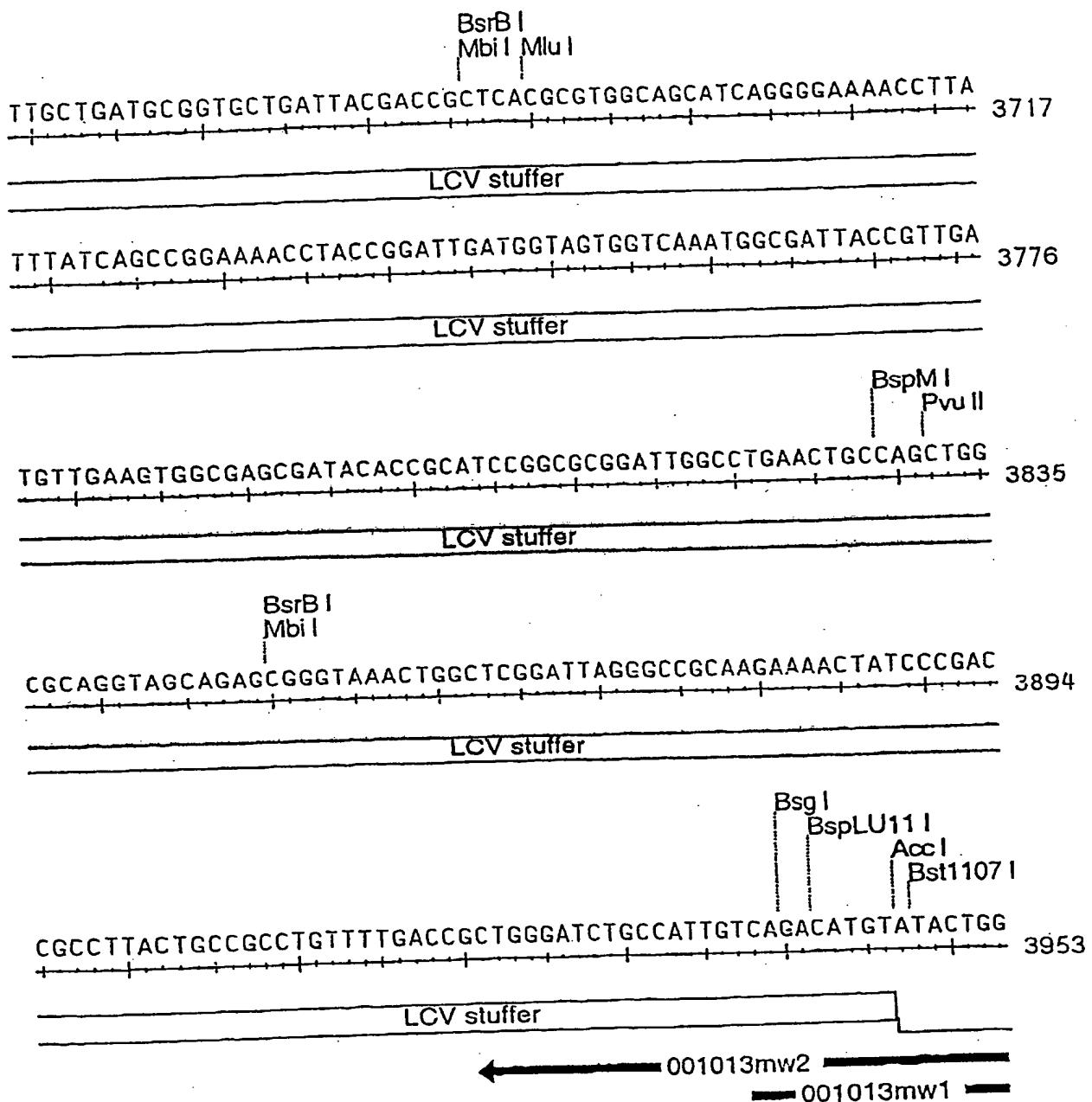


Fig. 4L

Bbs I

CTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCC 4012

Kappa Cns

001013mw1 →

Xmn I

TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGT 4071

Kappa Cns

GGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGG 4130

Kappa Cns

BbvC I
Bpu10 I

ACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAACAC 4189

Kappa Cns

Alw N I
Bpu10 I

AAAGTATATGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCCCGTACAAAGAGCTT 4248

Kappa Cns

Fig. 4M

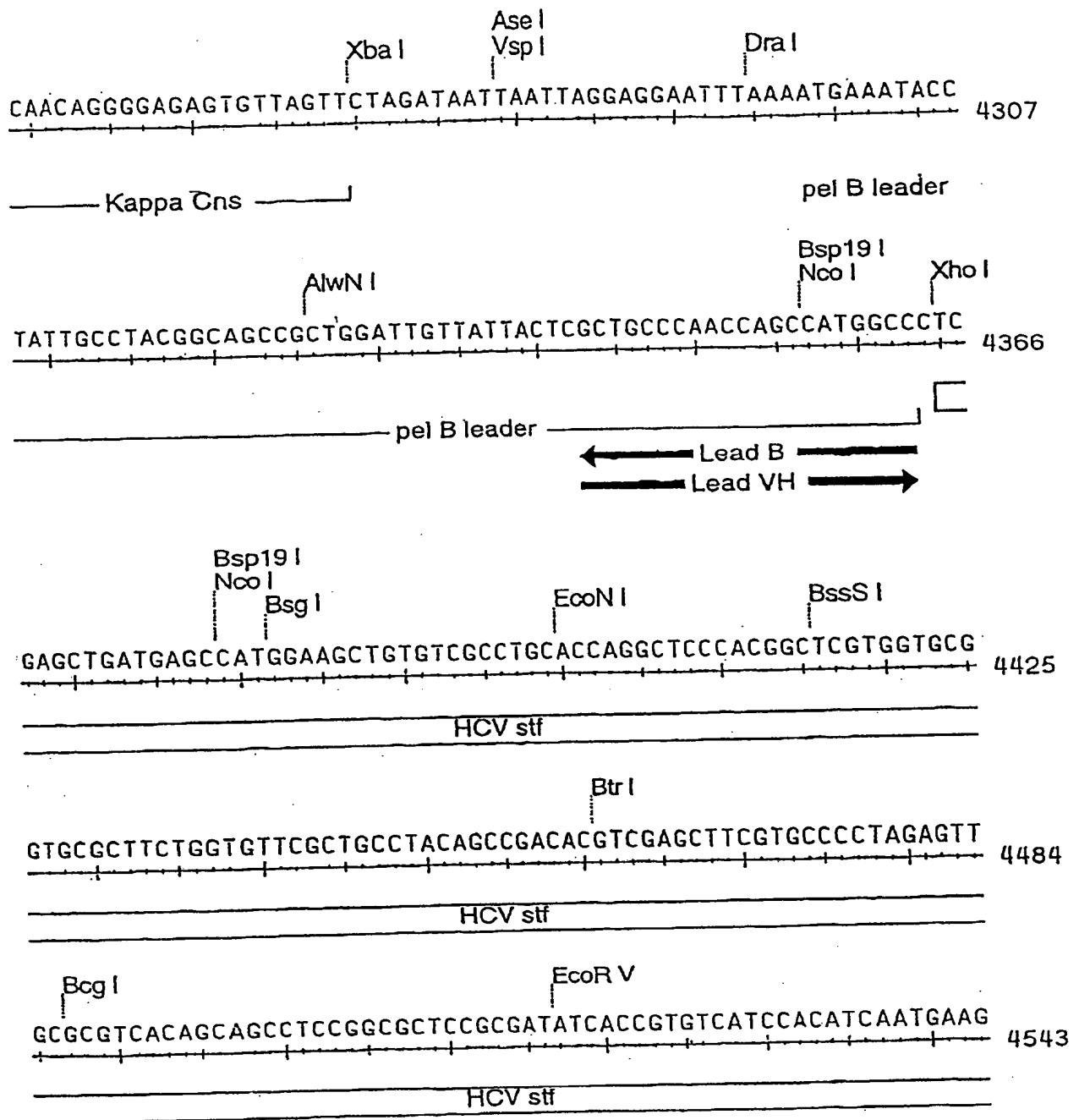


Fig. 4N

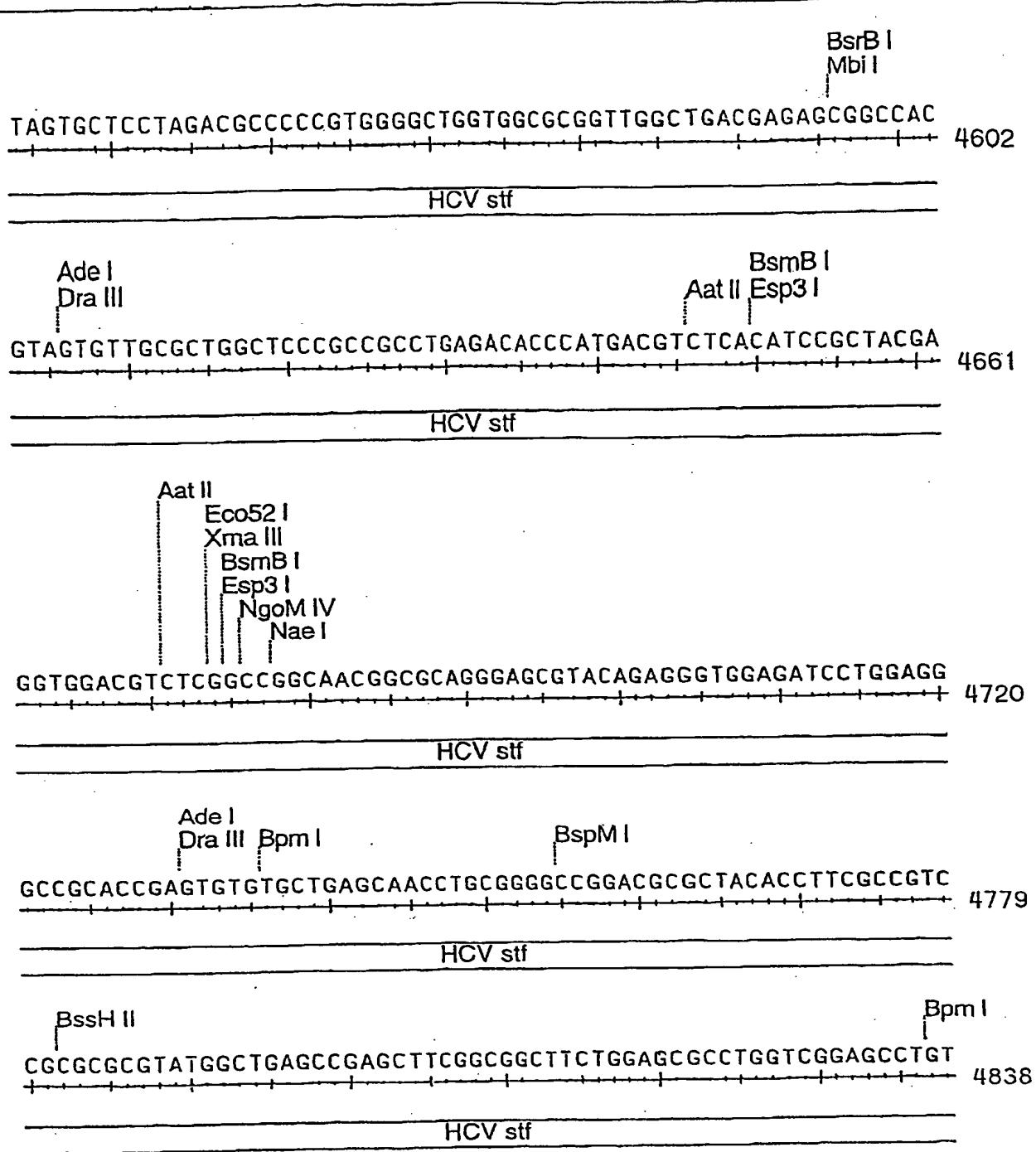


Fig. 4O

Detailed description: The figure displays five horizontal lines representing different regions of the HCV stf genome. Each line is marked with vertical tick marks indicating restriction enzyme cleavage sites. Above each line, the corresponding restriction enzymes are listed. The regions are numbered on the right side.

- Region 1:** BssS I, HCV stf, Eco57 I, Stu I, Ear I. The sequence starts at position 4897.
- Region 2:** Bgl II, Eco57 I, HCV stf, Stu I, Ear I. The sequence starts at position 4956.
- Region 3:** HCV stf, Pvu II, BstX I, Bsg I. The sequence starts at position 5015.
- Region 4:** HCV stf, Pvu II, BstX I, Bsg I. The sequence starts at position 5074.
- Region 5:** HCV stf, BspM I, Eco47 III. The sequence starts at position 5133.
- Region 6:** HCV stf, PspOM I, Bbs I, Apa I. The sequence starts at position 5192.

Fig. 4P

BseR I

EcoN I

CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
5251

Age I
PinA I

Tth111 I

Kas I
Nar I
Ehe I
Bbe I

AGGACTACTTCCCCAACCGGTGACGGTGTGCGTGGAACTCAGGCGCCCTGACCAGCGGC
5310

Alw44 I
ApaL I

Bsu36 I

BbvCI
Bpu10I
BpmI
BstE II

GTCACACCTTCCC GGCTGT CCTACAGT CCTCAGGACTCTACTCCCTCAGCAGCGTG GTGGT
5369

BstX I

GACCGTGCCTCCAGCAGCTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
5428

Bcu I
SpeI

Bcu I
BalI
MscI

CCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTTAGTGGC
5487

Fig. 4Q

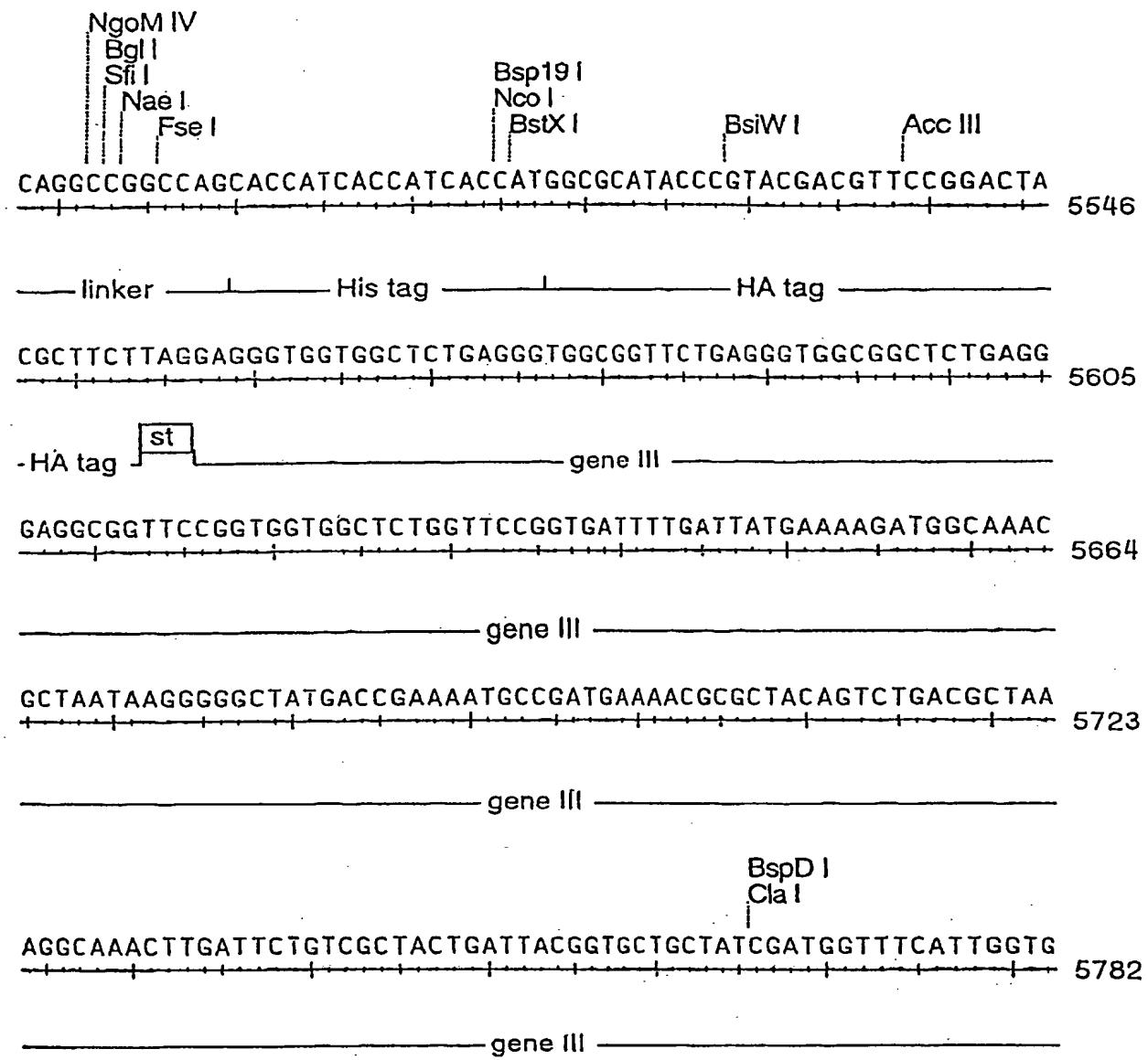


Fig. 4R

ACGTTCCGGCCTGCTAATGGTAATGGTGCCTACTGGTGATTTCGCTGGCTCAATTCC 5841
 gene III

CAAATGGCTCAAGTCGGTGACGGTGATAATTACACCTTAATGAATAATTCCGTCAATA 5900
 gene III

TTTACCTTCCCTCCCTCAATCGGTTGAATGTCGCCCTTTGTCTTAGCGCTGGTAAAC 5959
 gene III

CATATGAATTCTATTGATTGTGACAAAATAAACTTATTCCGTGGTGTCTTGCCTT 6018
 gene III

CTTTATATGTTGCCACCTTATGTATGTATTCTACGTTGCTAACATACTGCGTAA 6077
 gene III
 ← 991222nw3 →

Fig. 4S

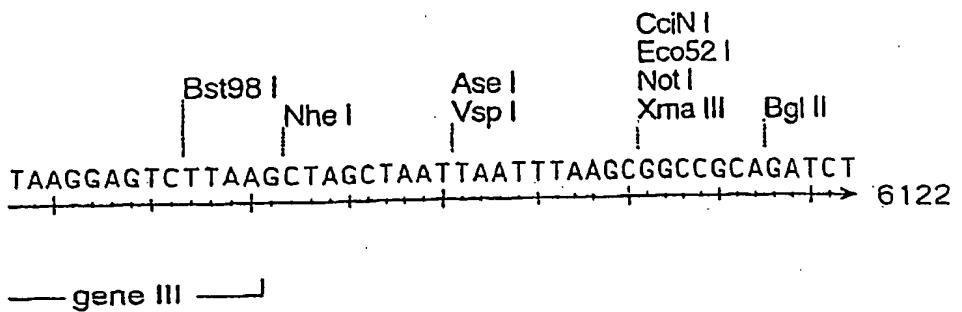


Fig. 4T

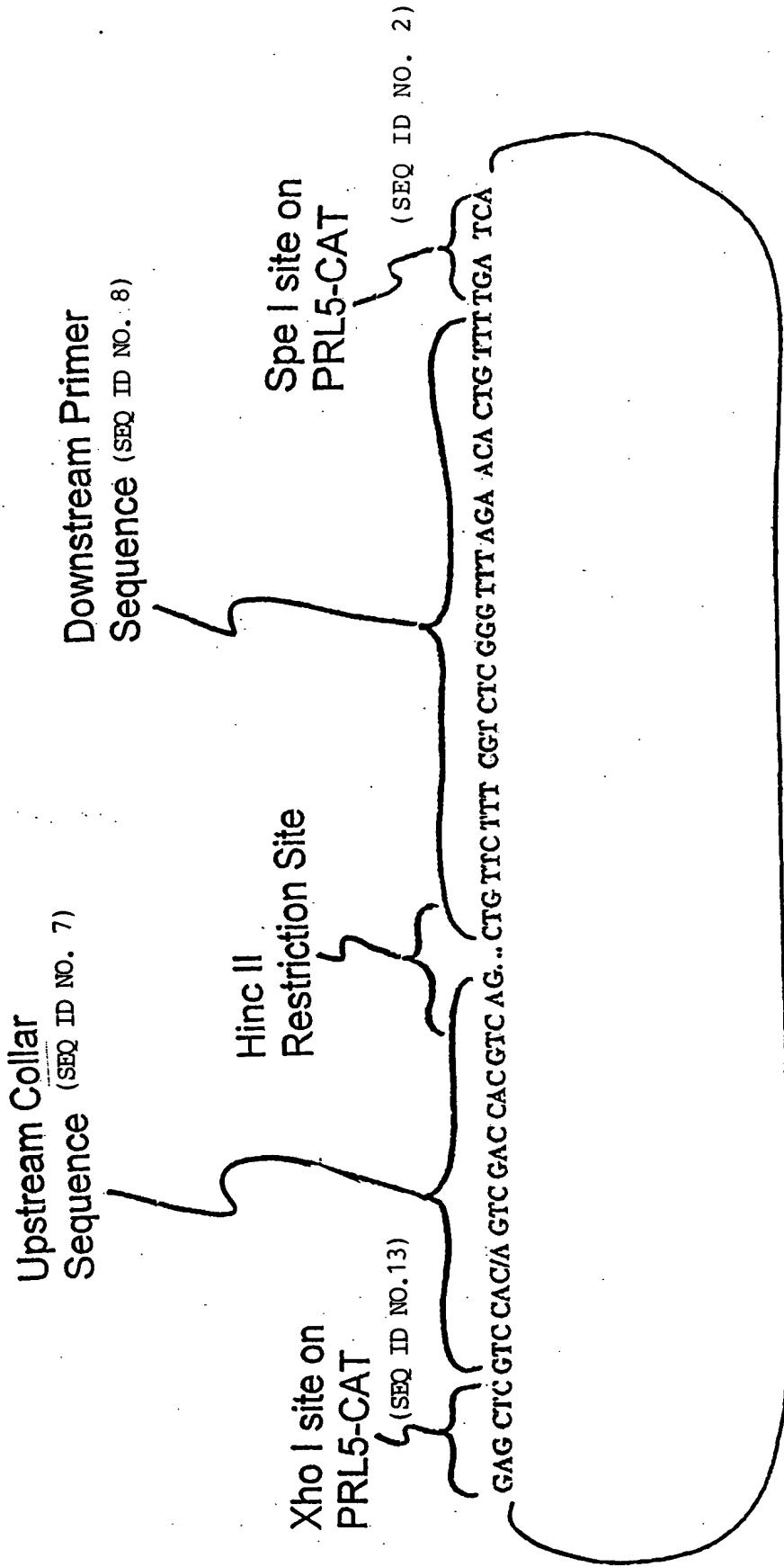


FIG. 6B

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